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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/056,884

DATE: 02/15/2002
 TIME: 14:40:39

Input Set : A:\EP.txt
 Output Set: N:\CRF3\02152002\J056884.raw

3 <110> APPLICANT: Bristol-Myers Squibb Company
 5 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
 BETA-SUBUNIT,

6 K+betaM2

8 <130> FILE REFERENCE: D0076 NP

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/056,884

C--> 10 <141> CURRENT FILING DATE: 2002-01-24

10 <150> PRIOR APPLICATION NUMBER: US 60/263,872

11 <151> PRIOR FILING DATE: 2001-01-24

13 <150> PRIOR APPLICATION NUMBER: US 60/269,794

14 <151> PRIOR FILING DATE: 2001-02-14

16 <160> NUMBER OF SEQ ID NOS: 73

18 <170> SOFTWARE: PatentIn version 3.0

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 3468

22 <212> TYPE: DNA

23 <213> ORGANISM: Homo sapiens

25 <220> FEATURE:

26 <221> NAME/KEY: CDS

27 <222> LOCATION: (515)..(1798)

29 <400> SEQUENCE: 1

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 34 gatctggcag ctctgtgtat ttcagtcagg ttccacaatg aaacctgaca ataatggtaa 180
 36 aaaccaatac ggacatctga gtaactgggg aattggcctg ccttgcattg gagcttgatg 240
 38 gaagattgga tatagacgag ttgattatat tttatgaagt agcagctcac taccatccac 300
 40 catccagggt ttaaactact ttttcagcat cacttcacct gtggactcct atacattttg 360
 42 atttcttggg ggaaaaatac tgggataaga ggaggtcatt tttaataag ttagcatcct 420
 44 tttccctttc ttacaagttg atccaaaagg taaggctgtg actccattgg attgcacctt 480
 46 taaatcaaaa tagcagcagc agaagaaagg gaca atg gct ctg agt gga aac tgt 535
 47 Met Ala Leu Ser Gly Asn Cys
 48 1 5
 50 agt cgt tat tat cct cga gaa caa ggg tcc gca gtt ccc aac tcc ttc 583
 51 Ser Arg Tyr Tyr Pro Arg Glu Gln Gly Ser Ala Val Pro Asn Ser Phe
 52 10 15 20
 54 cct gag gtg gta gag ctg aat gtc ggg ggt caa gtt tat ttt act cgc 631
 55 Pro Glu Val Val Glu Leu Asn Val Gly Gly Gln Val Tyr Phe Thr Arg
 56 25 30 35
 58 cat tcc aca ttg ata agc atc cct cat tcc ctc ctg tgg aaa atg ttt 679
 59 His Ser Thr Leu Ile Ser Ile Pro His Ser Leu Leu Trp Lys Met Phe
 60 40 45 50 55
 62 tcc cca aag aga gac acg gct aat gat cta gcc aag gac tcc aag gga 727
 63 Ser Pro Lys Arg Asp Thr Ala Asn Asp Leu Ala Lys Asp Ser Lys Gly
 64 60 65 70

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66 agg ttt ttc att gac aga gat gga ttc ttg ttc cgt tat att ctg gac      775
67 Arg Phe Phe Ile Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp
68              75              80              85
70 tat ctc agg gac agg cag gtg gtc ctg cct gat cac ttt cca gaa aaa      823
71 Tyr Leu Arg Asp Arg Gln Val Val Leu Pro Asp His Phe Pro Glu Lys
72              90              95              100
74 gga aga ctg aaa agg gaa gct gaa tac ttc cag ctg cca gac ttg gtc      871
75 Gly Arg Leu Lys Arg Glu Ala Glu Tyr Phe Gln Leu Pro Asp Leu Val
76              105              110              115
78 aaa ctg ctg acc ccc gat gaa atc aag caa agc cca gat gaa ttc tgc      919
79 Lys Leu Leu Thr Pro Asp Glu Ile Lys Gln Ser Pro Asp Glu Phe Cys
80 120              125              130              135
82 cac agt gac ttt gaa gat gcc tcc caa gga agc gac aca aga atc tgc      967
83 His Ser Asp Phe Glu Asp Ala Ser Gln Gly Ser Asp Thr Arg Ile Cys
84              140              145              150
86 ccc cct tcc tcc ctg ctg cct gcc gac cgc aag tgg ggt ttc att act      1015
87 Pro Pro Ser Ser Leu Leu Pro Ala Asp Arg Lys Trp Gly Phe Ile Thr
88              155              160              165
90 gtg ggt tac aga gga tcc tgc acc ttg ggc aga gag gga cag gca gat      1063
91 Val Gly Tyr Arg Gly Ser Cys Thr Leu Gly Arg Glu Gly Gln Ala Asp
92              170              175              180
94 gcc aag ttt cgg aga gtt ccc cgg att ttg gtt tgt gga agg att tcc      1111
95 Ala Lys Phe Arg Arg Val Pro Arg Ile Leu Val Cys Gly Arg Ile Ser
96              185              190              195
98 ttg gca aaa gaa gtc ttt gga gaa act ttg aat gaa agc aga gac cct      1159
99 Leu Ala Lys Glu Val Phe Gly Glu Thr Leu Asn Glu Ser Arg Asp Pro
100 200              205              210              215
102 gat cga gcc cca gaa aga tac acc tcc aga ttt tat ctg aaa ttc aag      1207
103 Asp Arg Ala Pro Glu Arg Tyr Thr Ser Arg Phe Tyr Leu Lys Phe Lys
104              220              225              230
106 cac ctg gaa agg gct ttt gat atg ttg tca gag tgt gga ttc cac atg      1255
107 His Leu Glu Arg Ala Phe Asp Met Leu Ser Glu Cys Gly Phe His Met
108              235              240              245
110 gtg gcc tgt aac tca tcg gtg aca gca tct ttc atc aac caa tat aca      1303
111 Val Ala Cys Asn Ser Ser Val Thr Ala Ser Phe Ile Asn Gln Tyr Thr
112              250              255              260
114 gat gac aag atc tgg tca agc tac act gaa tat gtc ttc tac cgt gag      1351
115 Asp Asp Lys Ile Trp Ser Ser Tyr Thr Glu Tyr Val Phe Tyr Arg Glu
116              265              270              275
118 cct tcc aga tgg tca ccc tca cac tgc gat tgc tgc tgc aag aat ggc      1399
119 Pro Ser Arg Trp Ser Pro Ser His Cys Asp Cys Cys Cys Lys Asn Gly
120 280              285              290              295
122 aaa ggt gac aaa gaa ggg gag agc ggc acg tct tgc aat gac ctg tcc      1447
123 Lys Gly Asp Lys Glu Gly Glu Ser Gly Thr Ser Cys Asn Asp Leu Ser
124              300              305              310
126 aca tct agc tgc gac agc cag tct gag gcc agc tct ccc cag gag acg      1495
127 Thr Ser Ser Cys Asp Ser Gln Ser Glu Ala Ser Ser Pro Gln Glu Thr
128              315              320              325
130 gtc atc tgt ggt ccc gtg aca cgc cag acc aac atc cag act ctg gac      1543

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131 Val Ile Cys Gly Pro Val Thr Arg Gln Thr Asn Ile Gln Thr Leu Asp
132          330          335          340
134 cgt ccc atc aag aag ggc cct gtc cag ctg atc caa cag tca gag atg      1591
135 Arg Pro Ile Lys Lys Gly Pro Val Gln Leu Ile Gln Gln Ser Glu Met
136          345          350          355
138 cgg cgg aaa agc gac tta ctc cgg att ctg act tca ggc tcc agg gaa      1639
139 Arg Arg Lys Ser Asp Leu Leu Arg Ile Leu Thr Ser Gly Ser Arg Glu
140 360          365          370          375
142 tcg aac atg agc agc aaa aaa aaa gct gtt aaa gaa aag ctc tca att      1687
143 Ser Asn Met Ser Ser Lys Lys Lys Ala Val Lys Glu Lys Leu Ser Ile
144          380          385          390
146 gag gag gag ctg gag aaa tgt atc cag gat ttc cta aaa aaa aaa att      1735
147 Glu Glu Glu Leu Glu Lys Cys Ile Gln Asp Phe Leu Lys Lys Lys Ile
148          395          400          405
150 cca gat cgg ttt cct gag aga aaa cat cct tgg caa tct gaa ctt tta      1783
151 Pro Asp Arg Phe Pro Glu Arg Lys His Pro Trp Gln Ser Glu Leu Leu
152          410          415          420
154 agg aag tat cat cta taaggaggagg ctggggggcgg ggaaaaaaaa aaaaaagagt      1838
155 Arg Lys Tyr His Leu
156          425
158 cattttgaaa ttaacctcat aaaaggaatt catatttttaa aggaaaaaaaa tacaactaat      1898
160 gatgcacatt tottagaaca caatagcca ttgatatact actgcctact ttacctagtt      1958
162 caccttaaca tgtaaatcca cagggtagat ttctttctag atgtggaagt acaagaaaaat      2018
164 cttttttagt tattgtttt tttacttcgt cccatgtgct aactatctta tatataatga      2078
166 gagccagcta cgtaaaagta gctgagaggc cttgggagtc atttatccca aactgggttt      2138
168 tttctctcat ccttctacct cctcctttg aatgagggta tggtagaaaa agatctggcc      2198
170 caatggcata agtttggaat ttttaatttt ggtttttcct tttgtttatg gggttggggg      2258
172 gaatggcaga tttatatgac ttttactca aatctatatg tgccagtta tattgactcc      2318
174 gtatgcatga gtatttgtgc aacacaagca caactaagta tgtatataca catgacgcac      2378
176 acgatgccag ggcctagacc tccaagggc tgtgtctctg ctcccagcag ccctctctta      2438
178 gaatatttca gatggatgag cttctgactc tttcttaaaa ttcttttggg aagatttccc      2498
180 agcctttcct cacaacactt totaacatca aatgactctc atcatcaaca aattgtattc      2558
182 cttattgtga aattaatacc ctcaggctcc attttactgc tttgctcttt gtctgcatta      2618
184 agagaggatg aggagagctg gtcaaacatt ccttgtgtta aaaaaatcaa acattcatat      2678
186 ccacaaaatt ttctgctaaa tgactccaca ctcagccttc tctaccctga actgaattat      2738
188 cacccttttc tccatgtttt cagagttcct actgcccaca gtttaatggt gtggcctttc      2798
190 cacataatcc acattaagtt ctgtgttcct gtgttggtgt ggaactaagg acaacacaca      2858
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196 gtttttggtt gcctttggga ttcgggcttt ggctgtgcc atgctaggat ttagctgtgt      3038
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200 agatttctaa atgaaactat ctttttcaat tacatcctga cttgtataga cacagccaaa      3158
202 aagaaactgt taatagccat ccgtccatgt aactctgtat ttactaagg tacciaatagc      3218
204 tctttcatag acttgtgcta caagaaggtt aaaagaccag ttttattttc agcattcctc      3278
206 atgcatttca gtgtaacca aaaaataatt tgtcaattaa tagttgtgtg ccaagcactc      3338
208 ctaatttggt ttattgcgtg tgtgtgcatg tgtgtatgtg tatcacaggt aataaaggca      3398
210 attggatgat taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      3458
212 aaaaaaaaaa
215 <210> SEQ ID NO: 2

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216 <211> LENGTH: 428

217 <212> TYPE: PRT

218 <213> ORGANISM: Homo sapiens

220 <400> SEQUENCE: 2

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227          20          25          30
230 Gly Gln Val Tyr Phe Thr Arg His Ser Thr Leu Ile Ser Ile Pro His
231          35          40          45
234 Ser Leu Leu Trp Lys Met Phe Ser Pro Lys Arg Asp Thr Ala Asn Asp
235          50          55          60
238 Leu Ala Lys Asp Ser Lys Gly Arg Phe Phe Ile Asp Arg Asp Gly Phe
239 65          70          75          80
242 Leu Phe Arg Tyr Ile Leu Asp Tyr Leu Arg Asp Arg Gln Val Val Leu
243          85          90          95
246 Pro Asp His Phe Pro Glu Lys Gly Arg Leu Lys Arg Glu Ala Glu Tyr
247          100         105         110
250 Phe Gln Leu Pro Asp Leu Val Lys Leu Leu Thr Pro Asp Glu Ile Lys
251          115         120         125
254 Gln Ser Pro Asp Glu Phe Cys His Ser Asp Phe Glu Asp Ala Ser Gln
255          130         135         140
258 Gly Ser Asp Thr Arg Ile Cys Pro Pro Ser Ser Leu Leu Pro Ala Asp
259 145         150         155         160
262 Arg Lys Trp Gly Phe Ile Thr Val Gly Tyr Arg Gly Ser Cys Thr Leu
263          165         170         175
266 Gly Arg Glu Gly Gln Ala Asp Ala Lys Phe Arg Arg Val Pro Arg Ile
267          180         185         190
270 Leu Val Cys Gly Arg Ile Ser Leu Ala Lys Glu Val Phe Gly Glu Thr
271          195         200         205
274 Leu Asn Glu Ser Arg Asp Pro Asp Arg Ala Pro Glu Arg Tyr Thr Ser
275          210         215         220
278 Arg Phe Tyr Leu Lys Phe Lys His Leu Glu Arg Ala Phe Asp Met Leu
279 225         230         235         240
282 Ser Glu Cys Gly Phe His Met Val Ala Cys Asn Ser Ser Val Thr Ala
283          245         250         255
286 Ser Phe Ile Asn Gln Tyr Thr Asp Asp Lys Ile Trp Ser Ser Tyr Thr
287          260         265         270
290 Glu Tyr Val Phe Tyr Arg Glu Pro Ser Arg Trp Ser Pro Ser His Cys
291          275         280         285
294 Asp Cys Cys Cys Lys Asn Gly Lys Gly Asp Lys Glu Gly Glu Ser Gly
295          290         295         300
298 Thr Ser Cys Asn Asp Leu Ser Thr Ser Ser Cys Asp Ser Gln Ser Glu
299 305         310         315         320
302 Ala Ser Ser Pro Gln Glu Thr Val Ile Cys Gly Pro Val Thr Arg Gln
303          325         330         335
306 Thr Asn Ile Gln Thr Leu Asp Arg Pro Ile Lys Lys Gly Pro Val Gln
307          340         345         350
310 Leu Ile Gln Gln Ser Glu Met Arg Arg Lys Ser Asp Leu Leu Arg Ile

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311          355          360          365
314 Leu Thr Ser Gly Ser Arg Glu Ser Asn Met Ser Ser Lys Lys Lys Ala
315          370          375          380
318 Val Lys Glu Lys Leu Ser Ile Glu Glu Glu Leu Glu Lys Cys Ile Gln
319 385          390          395          400
322 Asp Phe Leu Lys Lys Lys Ile Pro Asp Arg Phe Pro Glu Arg Lys His
323          405          410          415
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331 <211> LENGTH: 769
332 <212> TYPE: DNA
333 <213> ORGANISM: Homo sapiens
335 <400> SEQUENCE: 3
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340 caatggctct gagtggaac tgtagtcgtt attatcctcg agaacaagg tccgcagttc      180
342 ccaactcctt cctgaggtg gtagagctga atgtcgggg tcaagtttat ttactcgcc      240
344 attccacatt gataagcatc cctcattccc tcctgtggaa aatgttttcc ccaaagagag      300
346 acacggctaa tgatctagcc aaggactcca agggaaggtt ttctattgac agagatggat      360
348 tcttgttccg ttatattctg gactatctca gggacaggca ggtggtcctg cctgatcact      420
350 ttccagaaaa aggaagactg aaaagggaag ctgaatactt ccagctccca gacttggtca      480
352 aactcctgac ccccgatgaa atcaagcaaa gccagatga attctgccac agtgactttg      540
354 aagatgcctc ccaaggaaagc gacacaagaa tctgcccccc ttccctcctg ctcctgccc      600
356 accgcaagtg gggtttcatt actgtgggtt acagaggatc ctgcaccttg ggcagagagg      660
358 gacagcgaga tgccaagttt cggagagttc cccggatttt ggtttggtga aggatttcct      720
360 tggcaaaaga agtctttgga gaaactttga atgaaagcag agaccctga      769
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364 <211> LENGTH: 237
365 <212> TYPE: PRT
366 <213> ORGANISM: Homo sapiens
368 <400> SEQUENCE: 4
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373 Asn Val Gly Gly His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg
374          20          25          30
376 Tyr Pro Asp Ser Met Leu Gly Ala Met Phe Gly Gly Asp Phe Pro Thr
377          35          40          45
379 Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu
380          50          55          60
382 Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro
383 65          70          75          80
385 Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr
386          85          90          95
388 Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr
389          100         105         110
391 Pro Met Asp Thr Phe Glu Glu Val Glu Leu Ser Ser Thr Arg Lys
392          115         120         125
394 Leu Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:574 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8